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(without alignments)
611.308 Million cell updates/sec
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Sequence 6, Appli
Sequence 57, Appli
Sequence 55, Appl
Sequence 58, Appl
Sequence 50, Appl
Sequence 50, Appl
Sequence 17, Appl
Sequence 11, Appl
Sequence 17, Appl
Sequence 60, Appli
Sequence 60, Appli
Sequence 6, Appli
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Sequence 54, Appl
Sequence 6, Appli
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2540
1 MKNNILVILLISLFINQIKS.......QCDFANFLSISLLLISYYLL 468
                                                                                                                           December 26, 2001, 10:35:29 ; Search time 9.67 Seconds
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1: /cgn2_6/ptodata/2/paa/PCT_NEW_COMB.pep:*

3: /cgn2_6/ptodata/2/paa/USO6_NEW_COMB.pep:*

3: /cgn2_6/ptodata/2/paa/USO8_NEW_COMB.pep:*

3: /cgn2_6/ptodata/2/paa/USO8_NEW_COMB.pep:*

3: /cgn2_6/ptodata/2/paa/USO8_NEW_COMB.pep:*

3: /cgn2_6/ptodata/2/paa/USO8_NEW_COMB.pep:*

7: /cgn2_6/ptodata/2/paa/USO8_NEW_COMB.pep:*

7: /cgn2_6/ptodata/2/paa/USO8_NEW_COMB.pep:*
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
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US-09-497-967-54

US-09-497-967-61

US-09-497-967-61

US-09-497-967-57

US-09-497-967-57

US-09-497-967-58

US-09-497-967-59

US-09-497-967-60

US-09-497-967-60

US-09-975-143-47

US-09-975-143-47

US-09-975-143-47

US-09-977-053-6

US-09-977-967-10
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Maximum Match 100%
Listing first 45 summaries

    protein search, using sw model

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Gapop 10.0 , Gapext 0.5
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Sequence:
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Gequence 7, Application US/09497967

GENERAL INFORMATION:
APPLICANT: Clark, Theodore G.
APPLICANT: Dickerson, Jr., Harry W.
APPLICANT: Lin, Tian-Long
ITTLE OF INVENTION: DIAGNOSTIC AND PROTECTIVE ANTIGEN GENE SEQUENCES OF
ITTLE OF INVENTION: LICHTHVOPHTHIRUS
FILE REFERENCE: 235.00170101
CURRENT APPLICATION NUMBER: 05/09497,967
CURRENT APPLICATION NUMBER: 60/131,121
PRIOR PAPLICATION NUMBER: 60/131,121
PRIOR PLING DATE: 1999-04-27
PRIOR PLING DATE: 1999-02-04
PRIOR PLING DATE: 1999-03-02
PRIOR PLING DATE: 1999-03-02
PRIOR PLING DATE: 1999-03-02
PRIOR PLING DATE: 1999-03-02
SPRIOR PLING DATE: 1999-03-02
SPRIOR FILING DATE: 1999-03-17
SEQ ID NOS: 102
SOFTWARE: Patentin Ver. 2.1
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18, Appl
106, Appl
106, App
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100.0%; Score 2540; DB 5;
Best Local Similarity 100.0%; Pred. No. 7.9e-199;
Matches 468; Conservative 0; Mismatches 0;
   US-09-500-746-19
US-09-898-570-11
US-09-898-570-10
US-09-898-570-14
US-09-898-570-14
US-09-898-570-14
US-09-898-570-14
US-09-898-570-14
US-09-898-570-14
US-09-801-368-106
US-09-91-496-52
US-09-91-496-52
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US-09-91-496-52
US-09-91-496-52
US-09-866-987-21
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; ORGANISM: Ichthyophthirius multifiliis
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Best Local
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GENERAL INFORMATION:
APPLICANT: Clark, Theodore G.
APPLICANT: Dickerson, Jr., Harry W.
APPLICANT: Dickerson, Jr., Harry W.
APPLICANT: Lin, Than-Long
TITLE OF INVENTION: DIAGNOSTIC AND PROTECTIVE ANTIGEN GENE SEQUENCES OF
TITLE OF INVENTION: ICHTHYOPHTHIRUS
FILE REFERENCE: 235.0017010
CURRENT APPLICATION NUMBER: US/09/497,967
CURRENT FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: 60/111,121
PRIOR APPLICATION NUMBER: 60/112,372
PRIOR APPLICATION NUMBER: 60/122,372
PRIOR APPLICATION NUMBER: 60/122,372
PRIOR PLILING DATE: 1999-03-03-02
PRIOR FILING DATE: 1999-03-03-02
PRIOR FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 102
SOFTWARE: PATENTION NUMBER: 60/124,905
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241 CPDGTISAAGVNNWVAQNTECTNCAPNFYNNNAPNFNPGNSTCLPCPANKDYGAEATAGG 300
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                                                                                                                                                         361 VQGAVATAGGTATLIAQCALECPAGTVLTDGTTSTYKQAASECVKCAANFYTTKQTDWVA 420
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    CPDGTISAAGVNNWVAQNTECTNCAPNFYNNNAPNFNPGNSTCLPCPANKDYGAEATAGG
                            AATLAKQCNIACPDGTAIASGATNYVILQTECLNCAANFYFDGNNFQAGSSRCKACPANK
                                                                                                     99.7%; Score 2533; DB 5; Length 468; 99.8%; Pred. No. 2.9e-198; Live 0; Mismatches 1; Indels
                                                                                                                                                                                                                                  GIDTCTSCNKKLTSGAEANLPESAKKNIQCDFANFLSISLLLISYYLL 468
                                                                                                                                                                                                                                                                                                                                                                    Sequence 54, Application US/09497967
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Artificial Sequence
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Matches 467; Conservative
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APPLICANT: Clark, Theodore G.
APPLICANT: Clark, Theodore G.
APPLICANT: Dickerson, Jr., Harry W.
APPLICANT: Dickerson, Jr., Harry W.
APPLICANT: Lin, Tian-Long
TITLE OF INVENTION: DIAGNOSTIC AND PROTECTIVE ANTIGEN GENE SEQUENCES OF
TITLE OF INVENTION: DIAGNOSTIC AND PROTECTIVE ANTIGEN GENE SEQUENCES:
FILE REFERENCE: 235.00170101
CURRENT APPLICATION NUMBER: US/09/497,967
CURRENT FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: 60/131,121
PRIOR FILING DATE: 1999-04-27
PRIOR APPLICATION NUMBER: 60/131,372
PRIOR PLING DATE: 1999-03-04
PRIOR PILING DATE: 1999-03-04
PRIOR PLING DATE: 1999-03-04
PRIOR FILING DATE: 1999-03-07
SPRIOR PRILING DATE: 1999-03-07
SPRIOR PRILING DATE: 1999-03-07
SPRIOR PRILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 102.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   222 VAQATLGNDATITAQCNVACPDGTISAAGVNNWVAQNTE---CTNCAPNFYNN----N 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           117 NCRINFYNENAPNFNAGASTCTACPVNRVGGALTAGNAATIVAQCNVACPTGTALDDGVT 176
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                                                                                                                  1 MKNNILVILIISLFINQIKSANCPVGTETNTAGQVD----DLGTPANCVNCQKNFYYNNA 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                273 APN---FNPG-----NSTCLPCPANKDYGAEATAGGAATLAKQCNIACPDGTALAS
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                                                                                         361 VQGAVATAGGTATLIAQCALECPAGTVLTDGTTSTYKQAASECVKCAANFYTTKQTDWVA
                          45; Mismatches 139; Indels 114;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 442;
                                                                                                                                                                                                                421 GIDTCTSCNKKLTSGAEANLPESAKKNIQCDFANFLSISLLLISYYLL
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                                                                                                                                                                                                                                                                                                                                       US-09-497-967-6; Sequence 6, Application US/09497967; GENERAL INFORMATION:
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225 ATLGNDATITAQCNVA 240
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Matches 76; Conserv
                                                RESULT 5
US-09-497-967-57
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US-09-497-967-55
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APPLICANT: Clark, Theodore G.
APPLICANT: Dickerson, Jr., Harry W.
APPLICANT: Dickerson, Jr., Harry W.
APPLICANT: Lin, Tian-Long
TITLE OF INVENTION: DIAGNOSTIC AND PROTECTIVE ANTIGEN GENE SEQUENCES OF
TITLE OF INVENTION: ICHTHYOPHTHIRIUS
FILE REFERENCE: 235.00170101
CURRENT APPLICATION NUMBER: US/09/497,967
PRIOR APPLICATION NUMBER: 06/131,121
PRIOR APPLICATION NUMBER: 60/131,121
PRIOR APPLICATION NUMBER: 60/132,372
PRIOR PLING DATE: 1999-04-27
PRIOR PLING DATE: 1999-03-04
PRIOR PLING DATE: 1999-03-04
PRIOR PLING DATE: 1999-03-07
PRIOR PLING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 102
SOFTHARE: Patentin Ver. 2.1
LENGTH: 409
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                        380 LECPAGTVLTDGTTSTYKQAASECVKCAANFYTTKQTDWVAGIDTCTSCNKKLTSGAEAN 439
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              139 ACPVNRVGGALTAGNAATIVAQCNVACPTGTALDDGVTTDYVRSFTECVKCRLNFYYNGN 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   199 N--GNTP----FNPG------KSQCTPCPAIKPANVAQATLGNDATITAQCNVACPD 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      244 GIISAAGVNNWVAQNTE---CINCAPNFYNN----NAPN---FNPG-----NST 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     283 CLPCPANKDYGAEATAGGAATLAKQCNIACPDGTAIASGAT-NYVILQTECLNCAANFYF 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             342 DGNNFQAGSSRCKACPANKVQGAVATAGGTATLIAQCALECPAGTVLTDGTTSTYKQAAS 401
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31.6%; Score 801.5; DB 5; Length 409;
Best Local Similarity 39.5%; Pred. No. 4.8e-58;
Matches 187; Conservative 39; Mismatches 137; Indels 111;
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                                                                                         440 LPESAKKNIQC---DFANFLSISLLLISYYLL 468
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                                                                                                                                                              US-09-497-967-61; Sequence 61, Application US/09497967; GENERAL INFORMATION:
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APPLICANT: Dickerson, Jr. Haury W.
APPLICANT: Lin, Tian-Long
TITLE OF INVENTION: DIAGNOSTIC AND PROTECTIVE ANTIGEN GENE SEQUENCES OF
TITLE OF INVENTION: DIAGNOSTIC AND PROTECTIVE ANTIGEN GENE SEQUENCES OF
TITLE OF INVENTION: LITTLY OPPLICATION NUMBER: US/09/497,967
CURRENT APPLICATION NUMBER: 60/131,121
PRIOR FILING DATE: 1999-04-27
PRIOR PLING DATE: 1999-02-04
PRIOR PLING DATE: 1999-02-04
PRIOR PLING DATE: 1999-02-04
PRIOR PLING DATE: 1999-03-02
PRIOR PLING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 102
SOFTWARE: PATENTING DATE: 1999-03-17
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GENERAL INFORMATION:
APPLICANT: Clark, Theodore G.
APPLICANT: Clark, Theodore G.
APPLICANT: Lin, Tian-Long
TITLE OF INVENTION: DIAGNOSTIC AND PROTECTIVE ANTIGEN GENE SEQUENCES OF
TITLE OF INVENTION: DIAGNOSTIC AND PROTECTIVE ANTIGEN GENE SEQUENCES OF
TITLE OF INVENTION: DIAGNOSTIC AND PROTECTIVE ANTIGEN GENE SEQUENCES OF
TITLE OF INVENTION: LIGHTYOPHTHIRIUS
FILE REFERENCE: 235.00170101
CURRENT APPLICATION NUMBER: 05/09/497,967
CURRENT FILING DATE: 1999-04-27
PRIOR FILING DATE: 1999-03-02
PRIOR FILING DATE: 1999-03-02
PRIOR PELING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 102
SOFTWARE: PATENTIN VET. 2.1
SEQ ID NO 55
LENGTH: 72
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ilarity 100.0%; Pred. No. 3.1e-28;
Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TYPE: PRT
; ORGANISM: Ichthyophthirius multifillis
US-09-497-967-57
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US-09-497-967-55
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GENERAL INFORMATION:
APPLICANT: Clark, Theodore G.
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SEQ ID NO 56
LENGTH: 70
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| Sequence 60, Application US/09497967
| GENERAL INFORMATION:
| APPLICANT: Clark, Theodore G.
| APPLICANT: Dickerson, Jr., Harry W.
| APPLICANT: Lin, Tian-Long
| TITLE OF INVENTION: ICHTHYOPHTHIRUS
| TITLE OF INVENTION: ICHTHYOPHTHIRUS
| FILE REPERENCE: 235.00170101
| CURRENT FILING DATE: 2000-02-04
| PRIOR APPLICATION NUMBER: 60/131,121
| PRIOR APPLICATION NUMBER: 60/118,634
| PRIOR APPLICATION NUMBER: 60/118,634
| PRIOR APPLICATION NUMBER: 60/123,372
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GENERAL INCOMMATION:
GENERAL INCOMMATION:
APPLICANT: Clark, Theodore G.
APPLICANT: Lin, Tian-Long Tian-Lo
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                                                                        Gaps
                                                                                                                                     23 CPVGTETNTAGQVDDLGTPANCVNCQKNFYYNNAAAFVPGASTCTPCPQKKDAGAQPNPP 82
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Query Match
Best Local Similarity 100.0%; Pred. No. 1.2e-26;
Matches 72; Conservative 0; Mismatches 0; Indels
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US-09-497-967-58
Sequence 58, Application US/09497967
; SEGNERAL INFORMATION:
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Best Local Similarity 100.0
Matches 71; Conservative
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US-09-497-967-60
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Sequence 56, Application US/09497967

Sequence 56, Application US/09497967

GENERAL INFORMATION:
APPLICANT: Clark, Theodore G.
APPLICANT: Lin, Tian-Long
APPLICANT: Lin, Tian-Long
TITLE OF INVENTION: DIGHNYOHTHIRIUS
FILE REFERENCE: 235.0017010
FILE REFERENCE: 235.0017010
FILE REFERENCE: 235.0017010
CURRENT APLICATION NUMBER: 00/131,121
PRIOR APPLICATION NUMBER: 60/131,121
PRIOR APPLICATION NUMBER: 60/131,121
PRIOR PLING DATE: 1999-04-27
PRIOR FILING DATE: 1999-04-27
PRIOR FILING DATE: 1999-03-02

PRIOR FILING DATE: 1999-03-02

PRIOR FILING DATE: 1999-03-02

NUMBER OF SEQ ID NOS: 102

SOFTWARE: Patentin Ver. 2.1
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100.0%; Pred. No. 2.6e-24;
ative 0; Mismatches 0;
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100.0%; Pred. No. 2e-25;
tive 0; Mismatches 0.
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US-09-497-967-56
                                                                                                                                                                   GRGANISM: Ichthyophthirius multifilliis US-09-497-967-60
PRIOR FILING DATE: 1999-03-02
PRIOR APPLICATION NUMBER: 60/124,905
PRIOR FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 102
SOFTWARE: PATENTIN VEr. 2.1
SEQ ID NO 60
: LENGTH: 72
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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Best Local Similarity 100.
Matches 72; Conservative
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Best Local Similarity
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                                  586 TTCCCATTTGAAAGTGGGAAACCATTCAAAATACAAGTACTGGTTGAACCTGACCA---- 641
                                                                                                                                                                                                                                                                                                               729 IGGIGACATAGACCICACCAGIGCITCATATACCATGATAAATCIGAAA----GGGGC 783
                                                                                                                                                                                                                                                                                                                                                              AGSSRCKACPANKVQGAVATAGGTATLIAQCALECPAG------TVLTDGT----- 392
                                                                                                                                                                                                                                                                     ---AGGAATLAKQCNIACPDG-----TAIASGATNYVILQTECLNCAANFYFDGNNFQ 347
                                                                                                                                                                                                                                                                                                                                                                                                          784 AGATTAAAAAAAAAAAAAAAGAATCTAAACCTTACATGTGTAAAGGTTTCATGTTCACTG 843
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      393 -----TSTYKQAASECVKCA--ANFYTTKQTDWVAG-IDTCTSCNKKLTSGAEA 438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              62 GASTCTPCPQKKDAGAQPNPPATANLVTQCNVKCPAGTALAGGATDYAAIITECVNCRIN 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 269 -YNNNAPNFNPGNST-----CLPCPANK-----DYGAEATAGGA----ATLAK 306
                                                                                192 NFYYNGNNGNTPFNPGKSQCTPCPAIKPANVAQATLGNDATITAQCNVACPDGTISAAGV
                                                                                                                            179 YVRSFTECVKCRLNF------YYNGNNGNTPFNPGKSQCTPCPAIKPANVAQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3567 ------AGATGAGCAGCCTGAGGCTGAGGACAGCCATGDCATGTATTGGTTT-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEPLICANT: BIOGEN, INC.
APPLICANT: BIOGEN, INC.
APPLICANT: GARBER, Ellen
APPLICANT: GARBER, Ellen
APPLICANT: GALDHANA, JOSE W.
TITLE OF INVENTION: HUMANIZED ANTI-LT-BETA-R ANTIBODIES
FILE REFERENCE: A100 PCT
CURRENT APPLICATION NUMBER: PCT/US01/32140
CURRENT FILING DATE: 2001-10-12
PRIOR FILING DATE: 2001-10-13
PRIOR FILING DATE: 2001-00-13
PRIOR FILING DATE: 2001-00-13
PRIOR FILING DATE: 2001-00-13
PRIOR FILING DATE: 2001-00-31
PRIOR FILING DATE: 2001-06-21
SPRIOR FILING DATE: 2001-06-21
SPRIOR FILING DATE: 2001-06-21
SPRIOR FILING DATE: PASSED for Windows Version 4.0
SEQ ID NO 33
FENENTIAL AREA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8.8%; Score 222.5; DB 1;
24.8%; Pred. No. 5.4e-10;
tive 11; Mismatches 208;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 33, Application PC/TUS0132140 ; GENERAL INFORMATION:
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; ORGANISM: Homo Sapien
PCT-US01-32140-33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 112; Conserv
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PCT-US01-32140-33
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APPLICANT: Lin, Tian-Long
TITLE OF INVENTION: DIAGNOSTIC AND PROTECTIVE ANTIGEN GENE SEQUENCES OF
TITLE OF INVENTION: IGHTHYOPHTHIRIUS
FILE REFERENCE: 235.001701010
CURRENT ELING DATE: 2000-02-04
CURRENT FILING DATE: 2000-02-04
PRIOR FILING DATE: 1999-04-07
PRIOR FILING DATE: 1999-04-07
PRIOR FILING DATE: 1999-04-07
PRIOR FILING DATE: 1999-02-04
PRIOR FILING DATE: 1999-03-07
PRIOR FILING DATE: 1999-03-07
PRIOR FILING DATE: 1999-03-07
PRIOR FILING DATE: 1999-03-07
PRIOR FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 102
SEQ ID NO 59
LENGTH: 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         312 CPDGTAIASGAINYVILQTECLNCAANFYFDGNNFQAGSSRCKACPANKVQGAVATAGGT 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        77 AQPNPPATANLVTQCNVKCPAGTAIAGGATDYAAIITECVNGRINFYNENAPNFNAGAST 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          545 AGCTGGATA-----ATAACTGGGGAAGGAAGAAAGACAGTC---------GGTT 585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      137 CTACPVNRVGGAL-TAGNA----ATIVAQCNVACPTGTALDDGVTTDXVRSFTECVKCRL 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               500 CACGCTTCAA----TGAGAACAAC-----AGGAGAGTCATTGTTTGCAATACAA 544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels 139; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23 CPVGTETNTAGQVDDLGTPANCVNCQKNFYYNNAAAFVPGASTC-----TPCPQKKDAG 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 11
US-09-975-143-47
Sequence 47, Application US/09975143
Sequence 47, Application US/09975143
GENERAL INFORMATION:
APPLICANT: HSU, Daniel, K.
APPLICANT: LIU, FU-Tong
APPLICANT: DOWLING, Christopher, A.
TITLE OF INVENTION: GIRECTIN EXPRESSION IS INDUCED IN
TITLE OF INVENTION: GIRHOTIC LIVER AND HEPATOCELLULAR CARCINOMA
FILE REFERENCE: DANISU.001C1
CURRENT FILING DATE: 2001-10-10
CURRENT FILING DATE: 2001-10-10
PRIOR APPLICATION NUMBER: US/09/975,143
PRIOR RILING DATE: 2000-03-29
NUMBER OF EXD ID NOS: 47
SOFTWARE: FESTEEQ for Windows Version 4.0
SEQ ID NO 47
LENGTH: 914
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14.7%; Score 373; DB 5; I
100.0%; Pred. No. 3.8e-24;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Ichthyophthirius multifillis US-09-497-967-59
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Best Local Similarity 100.
Matches 70; Conservative
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Best Local Similarity 25.7
Matches 123; Conservative
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US-09-975-143-47
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19;

Gaps

Length 4852;

Homo sapiens

; ORGANISM: HOMUS-09-886-055-431

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APPLICANT: Clark, Theodore G.
APPLICANT: Clark, Theodore G.
APPLICANT: Dickerson, Jr., Harry W.
APPLICANT: Lin, Tian-Long
APPLICANT: Lin, Tian-Long
TITLE OF INVENTION: DIAGNOSTIC AND PROTECTIVE ANTIGEN GENE SEQUENCES OF
TITLE OF INVENTION: LCHTHYOPHTHIRIUS
FILE REFERENCE: 235.00170,01
CURRENT APPLICATION NUMBER: US/09/497,967
CURRENT FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: 60/131,121
PRIOR APPLICATION NUMBER: 60/131,121
PRIOR APPLICATION NUMBER: 60/123,372
PRIOR PLING DATE: 1999-04-27
PRIOR PLING DATE: 1999-03-04
PRIOR PLING DATE: 1999-03-04
PRIOR PLING DATE: 1999-03-05
PRIOR PLING DATE: 1999-03-05
SOFTWARE: PALENTING DATE: 1999-03-17
SOFTWARE: PALENTING DATE: 1999-03-17
SOFTWARE: PALENTING DATE: 1999-03-17
SEQ ID NOS: 10.2
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APPLICANT: STRYER, LUBERT
APPLICANT: STRYER, LUBERT
APPLICANT: STRYER, LUBERT
APPLICANT: STRYER, LUBERT
ATTLE OF INVENTION: BLOSENSORS OF CHEMICAL SENSANTS
TITLE OF INVENTION: BLOSENSORS OF CHEMICAL SENSANTS
TITLE OF INVENTION: BLOSENSORS OF CHEMICAL SENSANTS
TITLE OF INVENTION: BLOSENSORS OF CHEMICAL SENSANTS
CURRENT APPLICATION NUMBER: 08/09/886,055
CURRENT FILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 522
NUMBER OF SEQ ID NOS: 522
SCOFTWARE: Patentin Ver. 2.1
SEQ ID NO 431
LENGTH: 975
                                                                                                                                                                 3832 GGAGACTGGGTCATCDCATAATAGATCAGGATCTTAGGCGCTTTCCA-----TGG 3881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              382 CPAGTVLTDGTTSTYKQAASECVKCAANFYTTKQTDWVAGIDTCTSCNKKLTSGAEANLP 441
                                                 3782 DCTTGCAAGTGATAG-TGACCCTGTCTCCCA-----CCGATGCAGACAAGGATGAT 3831
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           307 QCNIACPDGTAIASGATNYVILQTECLNCAANFYFDGNNFQAGSSRCK-ACPANKVQGAV 365
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                                                                                                            ---- ATAGGTATLIAQCALECPAGTVLTDGTTSTYKQAASECVKCAANFYTTKQTDWVAG
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8.3%; Score 212; DB 5;
Best Local Similarity 53.6%; Pred. No. 4.3e-11;
Matches 37; Conservative 12; Mismatches 20
                                                                                                                                                                                                                                                                                    3882 ITTCTGCTGDGTAGACAGTAATAAGTTGCGAA 3913
                                                                                                                                                                                                                               422 IDTCTSCNKKLTSGAEANLPESAKKNIQCDFA 453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; ORGANISM: Ichthyophthirius multifilliis
US-09-497-967-12
                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 12, Application US/09497967
GENERAL INFORMATION:
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61 AEATQKVQC 69
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US-09-886-055-431
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US-09-497-967-12
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SERVICE INFORMATION:

GENERAL INFORMATION:

APPLICANT: Winchester , Robert J.

APPLICANT: Winchester , Robert J.

APPLICANT: Gulko, Perrio

APPLICANT: Gulko, Perrio

TITLE OF INVENTION: USES OF INHIBITORS FOR THE ACTIVATION OF CXCR4 RECEPTOR BY SDF

TITLE OF INVENTION: TREATING RHEVMATOID ARTHRITIS

FILE REPERENCE: 0575/57005-B

CURRENT APPLICATION NUMBER: US/09/500,746

CURRENT FILING DATE: 2000-02-09

NUMBER OF SEQ ID NOS: 23

SOFTWARE: Patentin version 3.1

SEQ ID NO 1.2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               352 CICATGGC----GIGA-----CTA-----TGACCGCTATGTGGCT----GTGTG 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         375 IAQCALECPA--GTVLTDGTTSTYKQAASECVKCAANFYTTKQTDWVAGIDTCTSCNKKL 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 384 CAACCCICTACGGIACCCICTCCTCATGAACCGCAGGGITT-----GCTTATICAIGG 436
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          46 NANGGGGTGCNTNGGNNNAGANANTGN-----NTGGA---GAANGACA----ANGGG 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                              308 TCC------TCTACCTGACCCTGATTGGAGGGAATTCTTCCTGCTGGGT 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        316 -TAIASGATNYVILQTECLNCAANFYFDGNNFQAGSSRCKACPANKVQGAVATAGGTATL 374
                                                                                                                                                                       83 ATANLVIQCNVKCPAGTAIAGGAIDYAAIITECVNCRINFYNENAPNFNAGASTCTACPV 142
                                                                                                                                                                                                            154 AIGGACICC---CGCCICCACACACACCAIGIACTICITGC---ICAGCCAGC-ICICCAI 206
                                                                                                                                                                                                                                                      143 NRVGGALTAGNAATIVAQCNVACPTGTALDDGVTTDYVRSFTECVKCRLNFYYNGNNGNT 202
                                                                                                                                                                                                                                                                                                                                       203 PFNPGKSQCTPCPAIKPANVAQATLGNDATITAQCNVACPDGTISAAGVNNWVAQNTECT 262
                                                                                                             23 CPVGTETNIAGQVDDLGTPANCVNCQKNFYYNNAAAFVPGASTCIPCPQKKDAGAQPNPP 82
                                                                                                                                                                                                                                                                                                                                                                               ---AGGACCICCIGICCAAGGACAAGACCATITCCIICCIGGGCIGIGCAGIICAGAICI
                                                                                                                                                                                                                                                                                                                                                                                                                      263 NCAPNEYNNNAPNFNPGNSTCLPCPANKDYGAEAT ----AGGAATLAKQCNIACPDG--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               180; Indels 116;
Score 197.5; DB 5; Length 975; Pred. No. 1e-08;
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                                                                                                                                                                                                                                                                                                207 CATGGATACCATCTACATCT---GTATCACTGTCCCCAAGATGCTCC----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 186; DB 5;
Pred. No. 3.5e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9; Mismatches
                                                6; Mismatches
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Best Local Similarity 25.1%;
Matches 102; Conservative 9
             7.8%;
               Query Match 7.8%
Best Local Similarity 23.99
Matches 101; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; ORGANISM: Human
US-09-500-746-17
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US-09-500-746-17
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91 GGNGTCGNNGGAGCNGNTGTGAGTGGGAAGAA	138 TACPVNRVGGALTAGNAATIVAQCNVACPTGTALDDGVTTDYVRSFTECVKCRLNFYYNG 197	129 GTCAANAAGGACGAATATTTGCAA	198 NNGNTPFNPGKSQCTPCPAIKPANVAQATLGNDATITAQCNVACPDGTI 246		247 SAAGVINIWVAQNTECTINCAPNFYNNNAPNFNPGNSTCLPCPANKDYGAEATAGGAATL 304	213 AGTGINNGTIGACCCGAAGCNANAGIGGAINCAGGAGIAC-CIGGAGNNAACIAIGAACA 271	305 AKQCNIACPDGTAIASGATNYVILOTECLNCAANFYFDGNNFQAGSSRCKACPANKV 361	272 ANTAAGCGCAACAGCCAAAGAGGACTINCCGCTAGACCCACTCG 315	QGAVATAGGTATLIAQCALECPAGTVLTDGTTSTYKQAASECVKCAA 408		
91 GGNGTCGNNGGAC	38 TACPVNRVGGALT	29 GTCAANAAGGACG		155 NNGNNCAGGGCTG	47 SAAGVNNWVAQNT	:	05 AKOCNIACPD	72 ANTAAGCGCAACA	362 QGAVATAGGTATL	316AGGAAAA	
QQ	0y 1	Db 1	0y 1	Db 1:	0y 2,	Dp 5.	0у 3	Db 2.	Oy 3(3:	

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